

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

MasPar time 158.91 Seconds 861.291 Million cell updates/sec Fri May 14 08:07:02 1999; :uo

Lular output not generated.

>US-08-911-423-3 (1-1006) from US08911423.seq 1006 Description: Perfect Score: Title:

1 ATGGCACAGCAGCAGCGGT......ACAACGTCCTGACTGGGAAA 1006 TACCGTGTCGTGCCCCGGTA......TGTTGCAGGACTGACCCTTT Sequence: N.A.

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch

Searched:

188442 segs, 68026449 bases x 2

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq32
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part14 25:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part26 30:part28 34:part34 35:part38 31:part31 32:part37 38:part38 39:part39 40:part40

Mean 8.892; Variance 5.749; scale 1.547 istics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

						SUMMARIES		
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Res	Result	arc.	Query	Query	ä	Ę		, C
1		1	111111111111111111111111111111111111111	יייי איייייי	9 :	77	Description	Fred. NO.
υ	П	114	11.3	3327	30	T69936	Coprinus cinereus lac	1.47e-52
	7	96	9.5	2606	14	083527	P. falciparum E31a qe	2.05e-41
	٣	96	9.5	2606	32	T72895	Plasmodium E31a gene.	2.05e-41
	4	85	8.4	1581	22	T32233	Cuphea C14:0-ACP thio	1.08e-34
	S	71	7.1	533	38	V02890	Human HMGI-C aberrant	2.80e-26
	9	65	6.5	774	38	V02883	Human HMGI-C aberrant	9.86e-23
	7	59	5.9	797	38	V02898	Human HMGI-C aberrant	3.12e-19
	œ	43	4.3	91	σ	051746	Oligonucleotide probe	3.27e-10
υ	6	42	4.2	91	σ	051746	Oligonucleotide probe	1.14e-09
υ	10	42	4.2	204	-	N81164	Base substituted E.co	1.14e-09
	11	41	4.1	178	32	T76405	Human endothelin-1 an	3.97e-09
	12	38	3.9	204	7	N81164	Base substituted E.co	4.69e-08
υ	13	39	3.9	206	23	T27694	pGEM3Zf target fragme	4.69e-08

•	.69e-0	9e-0	.69e-0	.69e-0	.69e-0	.69e-0	4.69e-08	9e-0	.69e-0	.69e-0	9e-0	.69e-0	.69e-0	.69e-0	9e-0	.69e-0	.69e-0	.69e-0	.69e-0	9e-0	.69e-0	.69e-0	.69e-0	.69e-0	0-a6	.69e-0	.69e-0	9e-0	.69e-0	.69e-0	0-a6	6-0
	DNA substrate for 5'	5' Nuclease substrate	Human TSH beta-chain	enco	uence from phage	hage M13tg910 used	T. hyo gene 6:lacz fu	cassette	sion cassette	encoding	aRhol g	obus 1	asmid	BSGFP expre	Ä	nstruct pGEM-hTR c	oAT-1 sequ	quence of plasmid	lermal growth f	encoding hGH, EG	Plasmid pinvi.	man type	asmid GS	d,	asmid gl	lactis/	WRG3169 enc	c	tro virus vector p	asmid	Plasmid pM16.	Retro virus vector p5
	34	17	2757	99	800	32	011381	36	36	13	36	3	27	34	8	8	57	4	51	7	34	8	59	ø	59	905	24	9685	7373	8122	081225	7373
	37	13	23	40	٣	m	~	12	12	25	38	40	7	39	35	35	16	σ	37	35	14	38	15	16	15	ဖ	33	38	12	20	20	12
	206	228	349	696	28	28	1380	61	75	02	13	21	68	69	급	1	4164	27	4283	28	53	4771	79	4933	9	82	28	83	030	10930	095	10970
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	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	42
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ALIGNMENTS

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Coprinus cinereus laccase loc1 genomic DNA.

Benzenediol.oxygen oxidoreductase; laccase; lignin; Kraft pulp; dye; fungus; polymerase chain reaction; papermaking; ss.

Coprinus cinereus (strain IFO 8371).

Key 1.851

exon /*tag* a //number=1
                                                                                                                                                        /cons_splice= (5/site:YES,3/site:YES)
/note= "The printed version of the sequence has the following splice junction sequences (with exon nucleotides shown in capitals and intron 5' site:GC/gt and 3' site:ag/TG"
                                                                                                                                                                                                                                                                                                                                                              /cons_splice= (5'site:NO,3'site:NO)
/note= "The printed version of the sequence has the
                                                                                                                                                                                                                                                                                       /cons_splice (5'site:YES,3'site:YES)
1101..1248
                                                                                                                        /codon_start= 726
852..906
  T
169936 standard; DNA; 3327 BP.
                                                                                                                                                       /number= 1
                                                                                                                                                                                                                                                           1024..1100
                               (first entry)
                                                                                                                                                                                                                                                                                                                                 1249..1316
                                                                                                                                              /*tag= b
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                     T69936;
21-JUL-1997
                                                                                                                                    intron
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New laccase from Coprinus strains - useful for polymerising lignin, depolymerising Kraft pulp, oxidising dyes and their precursors, etc. Claim 18; F19 1; 62pp; English.

The present sequence encodes a novel laccase, lcc1, isolated from Coprinus cinereus strain IFO 8371. This polypeptide is used coprinus cinereus strain IFO 8371. This polypeptide is used depolymerise a lignin or lignosulphate in solution; for in situ depolymerisation of Kraft pulp; for oxidising dyes or their precursors (particularly to prevent dye transfer between fabrics and in hair dyeing) and for polymerising or oxidising phenolic compounds (e.g. to precipitate phenolics from fruit juices to give a more stable product). It can also be used for soil detoxification. Use of the polypeptide avoids the need to use chlorine for lignin depolymerisation. It has better activity than known laccases under the alkaline conditions usually encountered in papermaking processes. A CDNA library from
                                                                                                                                                       /cons_splice= (5'site:NO,3'site:NO)
/note= "The printed version of the sequence has the following splice junction sequences (with exon nucleotides shown in capitals and intron nucleotides shown in lower case):
5' site:TG/qt and 3' site:ag/GT"
1753..2240
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/note= "The printed version of the sequence has the following splice junction sequences (with exon nucleotides shown in capitals and intron nucleotides shown in lower case):
5' site:AA/qt and 3' site:ag/CG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "The printed version of the sequence has the
following splice junction sequences (with exon nucleotides shown in capitals and intron
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/cons.splice= (5'site:YES,3'site:YES)
2321..2494
/*tag= k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotides shown in lower case):
5' site:TG/gt and 3' site:ag/TC"
5/T1..3327
/*tag= o
/number= 8
                          nucleotides shown in lower case):
5' site:TG/gt and 3' site:ag/GC"
1317..1697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-1995; US-002800.
(NOVO ) NOVO NORDISK BIOTECH INC.
(NOVO ) NOVO-NORDISK AS.
                                                                                           /number= 4
1698..1752
/*tag= h
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                                                                                                                                                                                                                                                                                                                                                                                                                                            'number= 6
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P-PSDB; W17973.
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IFO 8371 was prepared and subjected to PCR with oligonucleotides based on the conserved motifs in other fungal laccases. The amplification product was cloned and 7 subclones were produced and sequenced. They correspond to 3 different laccases designated loc1, 2 and 3. To isolate full-length DNA, a genomic DNA library of IFO 8371 was constructed. A digoxigenin-labelled probe was prepared by PCR using loc1 CDNA as a template and 32P-labelled probes from loc2 and 3 partial cDNA. These probes were used to screen the genomic library and two clones
                                                                                                                                                            were isolated, one containing the loci gene and the other containing the loc3 gene. No single clone contained the complete loc2 gene which was isolated from two partial clones.

N.B. The sequence presented in this record is the same as the version supplied electronically to the European Patent Office; it differs from the sequence printed in Figure 1 of the specification at some of the exon/intron boundaries. See features table.

Sequence 3327 BP; 770 A; 917 C; 811 G; 829 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 TITCCCAGTCAGGACGTTGTAAAACGACGCCCAGTGAATTGAATTAGGTGACGTATAG 947
                                                                                                                                                                                                                                                                                                                                                                                                                              402 tttcccagtcacgacgttgtaaaacgacggccagtgaattgaatttaggtgacactatag 461
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                083527;
22-SEP-1995 (first entry)
P. falciparum E31a gene.
Exrythrocyte binding ligand; E31a; binding domain; malaria; therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure: Page 51-52; 81pp; English.

Erythrocyte binding ligand (EBL) family genes were cloned from P. falciparum chromosome 7 subsequent libraries constructed during genetic studies of the chloroquine resistance locus. The 4 genes, EBL-e1 (083526), E31a (083527), EBL-e2 (083528) and Proj3 (083529), encode the proteins given in R70233-36, respectively. The binding domains of such proteins can be expressed e.g. in E. coli, yeast, nammalian, insect, and in vaccinia virus and adenovirus-infected cells, and provide protection against P. falciparum.

Sequence 2606 BP; 992 A; 351 C; 569 G; 694 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New erythrocyte binding domain polypeptide(s) - isolated from Plasmodium binding proteins, used in diagnosis, treatment and prevention of malaria
                                                                                                                                                                                                                                                                                                                                                 Length 3327;
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                                                                                                                                                                                                                                                                                                                                             Score 114; DB 30; Length 33
Pred. No. 1.47e-52;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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10-SEP-1994; U5-119677.

COSSH ) US DEPT HEALTH & HUMAN SERVICES.

Chitnis C, Miller LH, Peterson DS, Sim KL,

Wellems TE;

WPI: 95-123427/16.

P-PSDB; R70234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Q83527 standard; DNA; 2606 BP.
                                                                                                                                                                                                                                                                                                                                             Match 11.3%;
Local Similarity 97.5%;
Les 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; ss.
Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9507353-A.
16-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                 Query Match
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standard; cDNA; 533 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-1997.
21-DEC-1995; 048122.
21-DEC-1995; DE-048122.
                                                                   02-FEB-1995; US-383756.
05-JUN-1995; US-460898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue regeneration; ss
/*tag=
                                                                                                    (CALJ ) CALGENE INC.
Dehesh K, Hawkins D,
WPI; 96-371439/37.
P-PSDB; W02081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BULL/) BULLERDIEK J.
                                            01-FEB-1996; U01585
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DE19548122-A1.
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V02890
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Disclosure; Page 43: 96pp; English.

This sequence represents the E31a gene of Plasmodium. E31a belongs to the Diffy binding like (DBL) family of genes which have homology to the Diffy antigen binding like (DBL) family of genes modified and sialic acid binding protein (SABP) and sialic acid binding protein (SABP) conserved regions (see T72889 and T72888 respectively). The var (EML) of genes modified cytoadherence and antigenic variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture consportant after infected erythrocytes release merozoites. DABP and SABP (EVAL) are sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and comprise either a nucleotide sequence or encoded polypeptide of the CVAT-1, var-2, var-3 or var-1 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They compositions are used for the treatment and prevention of malaria. They care also used in the preparation of vaccines for inducing a protective immune response in a mammal to plasmodium merozoites (especially sequence 2606 BP; 992 A; 351 C; 569 G; 694 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caagcttacgtacgcgtgcatgcgacgtcatagctcttctatagtgtcacctaaattcaa 2514
                                                                                  Plasmodium E31a gene.

DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;

Duffy binding like gene; Duffy antigen binding protein; erythrocyte;

DABP; merozoite; malaria; var-1; var-2; var-7; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 909 CAAGCITACGTACGCGTGCATGCGACGTCATAGCTCTTCTATAGTGTCACCTAAATTCAA 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 96; DB 32; Length 2606;
Pred. No. 2.05e-41;
0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           New malaria vaccines - contains cysteine-rich DBL family protein binding domains homologous domains of the Duffy and sialic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-0CT-1996 (first entry)
Cuphea C14:0-ACP thioesterase cDNA clone MCT34 (CpFatB2).
Myristate; myristic acid; fatty acid; acyl-ACP thioesterase; seed oil; oilseed; vegetable oil; Brassica; transgenic plant;
                                                                                                                                                                                                                              /*tag= a
/note= "encodes residues 1-785 of W22480"
                                                                                                                                                                                                                                                                                                                                                         Su X;
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Chitnis C, Miller LH, Peterson DS, Sim KL,
                                                                                                                                                                                           Location/Qualifiers
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                .T 3
T72895 standard; cDNA; 2606 BP.
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T32233 standard; cDNA; 1581 BP
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Local Similarity 99.0%;
les 97; Conservative
                                                                  07-OCT-1997 (first entry)
                                                                                                                                                                                                               106..2460
                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                                                                                                                                                                     07-JUN-1996; U09508
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P-PSDB; W22480.
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                                                                                                                                                          Plasmodium; ss
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                                                                                                                                                                                                                                                                  WO9640766-A2.
                                                                                                                                                                                                                                                                                                                                                       Chitnis C,
Wellems TE
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Best Local S:
                                                   T72895;
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kits can reduce, block or stimulate angiogenesis or vascularisation and can improve vascular provision in myocardium damaged by infarction. Such proteins can also be used to treat endometriosis and tumours, for contraception (local or oral) and for tissue regeneration, especially in degenerating or damaged tissue. The regeneration method can be applied to tissues which are currently impossible or difficult to regenerate and the use of biological material with attendant risks of viral transmission and anaphylactic shock, is avoided.
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WPI: 97-333837/31.
DNA sequences representing aberrant forms of human high mobility group protein genes - useful for treatment of endometriosis and tumours, or for modulating vascularisation, etc claim 1; Fig 11; S8Pp; German.
V02880-V02898 are CDNA sequences that encode aberrant forms of the human high mobility group protein (HMG) gene, HMGI-C, which is located on chromosome 12. These sequences encode the DNA binding part of the translation product but not the protein binding domain. These proteins antibodies derived from these proteins or expression modulators of the HMGI-C protein can be used in kits to modulate vascular development. Such WMGI-C protein can be used in kits to modulate vascular development. Such and the protein contact of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High mobility group protein; HMGI-C; MAG; human; treatment; modulator; multiple tumour aberration growth gene; vascular development; angiogenesis; vascularisation; endometriosis; contraception
                                                                                                                                                                                               Recombinant prodn. of myristate in plant cells - using DNA with preferential activity on C14 fatty acids from Cuphea palustris, nutmeng and camphor, useful in detergent and food industries Example 1: Fig 1A-1E; 77pp; English.
A CDNA clone (T32233), designated MCT34 (pCpFatB2), codes for Cuphea palustris C14:0-ACP thioesterase (W02081), an enzyme that acts primarily on C14:0-ACP substrates, forming C14:0 (myristate). It was isolated from a developing seed cDNA library by screening with sequences encoding medium-chain acyl-ACP thioesterases from Cuphea hookeriana. Constructs for expression of clone MCT34 in plant seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     under the control of napin or oleosin regulatory regions were prepd. These allow high-level prodn. of myristate (useful in surfactants and foods) in plant cells, e.g. Brassica. Sequence 1581 BP; 418 A; 356 C; 410 G; 397 T;
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8.4%; Score 85; DB 22; Length 1581;
Best Local Similarity 98.9%; Pred. No. 1.08e-34;
Matches 86; Conservative 0: Mismatches 1. Trail (
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Voelker TA;
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1 ggctccggcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsv 60
   regeneration; ss.
                                                                                                          (BULL/) BULLERDIEK J.
                    Homo sapiens.
DE19548122-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaphylactic
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                                                                                                                          Bullerdiek
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Bullerdisk J.

Bussen - useful for treatment of endometriosis and contracted general forms of the human of tumours, or for modulating vascularisation, etc.

Claim J. Fig 4. 5Bpp; German.

Claim J. Fig 4. 5Bpp; German.

Cloim mobility group protein (HMG) gene, HMG1-C, which is located on high mobility group protein (HMG) gene, HMG1-C, which is located on this mobility group protein (HMG) gene, HMG1-C, which is located on translation product but not the protein binding domain. These proteins, antibodies derived from these proteins or expression modulators of the HMG1-C protein can be used in kits to modulate vascular development. Such the HMG1-C protein can also be used to treat endometriosis and tumours, for contracteption (local or oral) and for tissue regeneration, especially in degenerating or damaged tissue. The respeneration method can be applied to tissue which are currently impossible or difficult to regenerate and the last of the book, is and in a protein trisks of viral transmission and the manner of the protein the protein or and the protein to the protein the protein trisks of viral transmission and the manner of the protein the 
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                                                                                                                                                                                                                                                                                                                                                     High mobility group protein; HMGI-C; MAG; human; treatment; modulator; multiple tumour aberration growth gene; vascular development; anglogenesis; vascularisation; endometriosis; contraception
                                                                                                    708 ggcggccgctctagaggatccaagcttacgtacgcgtgcatgcgacgtcatagctcttct 767
                                                                       Gaps
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                                 Score 71; DB 38; Length 533;
Pred. No. 2.80e-26;
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 127 G;
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                                                                     0; Mismatches
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 146 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anaphylactic shock, is avoided.
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V02883 standard; cDNA; 774 BP.
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Human HMGI-C aberrant form 19.
                                                                                                                                                                                                                                                                                                                  08-MAY-1998 (first entry)
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   Ä;
                                 7.1%;
larity 98.6%;
Conservative
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21-DEC-1995; 048122.
21-DEC-1995; DE-048122.
(BULL/) BULLERDIEK J.
                                                                                                                                                                                                                                                                                                                                                                                                          tissue regeneration; ss
                                                                                                                                                                            521 atagtgtcaccta 533
                                                                                                                                                                                                949 ATAGTGTCACCTA 961
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BP;
                                                   Local Similarity
tes 72; Conser
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DE19548122-A1.
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 Sequence
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Matches
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high mobility group proced (MEG) gene, HMCI-C, which is located on chromosome 12. These sequences encode the DNA binding part of the translation product but not the protein bunding domain. These proteins, antibodies derived from these proteins or expression modulators of the HMGI-C protein can be used in kits to modulate vascular development. Such kits can reduce, block or stimulate angiogenesis or vascularisation and can improve vascular provision in myocardium demaged by infarction. Such proteins can also be used to treat endometriosis and tumours, for contraception (local or oral) and for tissue regeneration, especially in degenerating or damaged tissue. The regeneration method can be applied to tissues which are currently impossible or difficult to regenerate and the use of biological material with attendant risks of viral transmission and
                                                                                                                                                                     WPI; 97-333837/31.

DNA sequences representing aberrant forms of human high mobility group protein genes - useful for treatment of endometriosis and tumours, or for modulating vascularisation, etc claim 1; Fig 19; 58pp; German.

V02880-V02898 are cDNA sequences that encode aberrant forms of the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     889 GGGGGCCGCTCTAAAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCTTCT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Q5]735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q5]735-45 and Q5]747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   051746 standard; cDNA; 91 BP.
051746;
31-MAY-1994 (first entry)
Oligonuclectide probe MK14-A
Oligonuclectide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 38; Leuy...
Pred. No. 3.12e-19;
....matrhes 2; Indels
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Best Local Similarity 12.7%; Pred. No. 3.27e-10;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c'shock, is avoided.
797 BP; 267 A;
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01-DEC-1993.
24-MAY-1992; US-889551.
EBCT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 5.9%;
Best Local Similarity 96.8%;
Matches 61; Conservative
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26-JUN-1997.
21-DEC-1995; 048122.
21-DEC-1995; DE-048122.
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WPI; 93-378844/48.
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WO9640162-A1.
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Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T; WPI; 88-279927/40.
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.coli bear galactosidase. The wild type sequence was obtained as single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for
                                                                                                                                                                                                                                                                                                              Claim 3; Page 14; 23pp; English.

Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CS51735. It hybridized to all spp. of mycobacterial tested, but
cross reacted to a few non-mycobacterial spp. The probe may
be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
                                                                                                                                                                                                                                                                                - used for
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Random point mutations were introduced into the alpha fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                             Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                             New oligo:nucleotide probes specific for Mycobacteria – used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ssvhsyyvvhvvshhhsvhhvvhhvhvhvvhhvhhvhyhvyvsv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GCGCACAGCACGCCAGGCCGCACAAACGCGCCCATCGCCC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 91;
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187..204
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                4.2%; Score 42; DB 9; Lo
0.0%; Pred. No. 1.14e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                         standard; cDNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N81164 standard; DNA; 204 BP
                                                                                                                                                                                                                                         (BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-1990 (first entry)
                                                                                                                                31-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1987; US-034819.
                                                                                                                                                                                                                                                        Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1988.
30-MAR-1988; 105163
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                       Shank DD, Spears
WPI; 93-378844/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli
                                                         427 TTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-285123-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer_bind
                                                                                                                                                                               Synthetic
                                  ctc
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                        samples
                                                                                                        051746
                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                            RESULT
ID QE
AC QE
DE OI
DE OI
EN SE
PO OI
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ID N8
AC N8
DT 08
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A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific
                                                                                                                                                                                                                                                                                                                                                                                       76 ycdchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddh 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 ccttggcbbgccbcbbbcbgcbgbgbbbbtcbtgbgcbbbtbbtccbttctgbbbbbb 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                127 TCCCAAGCAGGAGGCGCCCAAGGGCCGCACCCGGGACCCCCGGTGGGGCGCTGACCCAGGC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tor the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary diseases, bronchitis and other airway diseases tharacterised by an inflammatory response. By eliminating adenosine from the antišense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine induced bronchoconstriction in patients with hyper-reactive airways. Sequence 178 BP; 0 A; 52 C; 46 G; 32 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NoV-1990 (first entry) asse substituted E.coli beta-galactosidase alpha-fragment. E.coli beta galactosidase alpha-fragment; base substitutions; ss. Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 yvybbbv-ynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvc 189
                                                                                                                                                                                                   108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human endothelin-1 antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 178;
                                                                                                                                                                                                                                                               Score 42; DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                           57; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Mismatches 16; Indels
                                                                                                                                                                                                      11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 32; 1 Pred. No. 3.97e-09;
                                                                                                                                                                                                                                                                                            Pred. No. 1.14e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 32;
                                                                                                                                                                                                17 G;
                                                                                                                                                                                                47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 38; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N81164 standard; DNA; 204 BP
N81164;
                                                                                                                                                                                                                                                                                            Best_Local Similarity 14.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
Metzger WJ, Nyce JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.1%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                  4.28;
                                                                                                                                                                                                   21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .T 11
T76405 standard; DNA; 178
T76405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 bgggbtcbbbbbc 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ||:| :::::|
95 ccGGGTGCGGCCC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1996; U09306
                                                                                                                                                                                                204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metzger WJ, Nyce, WPI; 97-051871/05.
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Query Match
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                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8888888888
                                                                                                                                                                           Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
Introducing random point mutations of molecules and screening.

This incorporation, completion of molecules and screening.

Disclosure: p; English.

Random point mutations were introduced into the alpha fragment of incorporation beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all single stranded template and an oligonucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which correct of the corporation in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; Page 265-266; 433pp; English.

Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (FFM) BN enzyme.

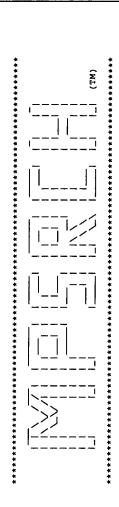
Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae Radi/RadiO complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or alternatively, microbial gene sequences. Cleavage products are compared to the cleavage products of reference gene sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pGEM32f target fragment.
p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella; Staphylococcus; identification; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage of nucleic acids to detect mutation(s) - allows detection esp. in human p53 gene, to identify strains of microorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method is used for detecting mutation in the human p53 gene; for
                                                                                                                                                                                                                                                                                                                                                                                                         17 G; 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|| | : ||::|:||||::||||::||||::||||
                                                                                                                                                     Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsdaaa 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fors L, Heisler LM, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 1; Length 204;
Pred. No. 4.69e-08;
27; Mismatches 7; Indels
                                       /function=multiple cloning site
187..204
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THIR-) THIRD WAVE TECHNOLOGIES INC.
Location/Qualifiers
19..69
                                                                                                                                                                                                                                                                                                                                                                                                         47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T27694 standard; DNA; 206 BP
                                                                                                                                                                                                                                                                                                                                                                                                        21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                     3.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  larity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1996 (first entry)
                              מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brow MAD, Dahlberg JE,
Oldenburg MC, Olive DM;
                                                                                                                                       (SUSO) SUOMEN SOKERI OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1994; US-337164.
09-MAR-1995; US-402601.
07-JUN-1995; US-484956.
30-AUG-1995; US-520946.
                                                                                                                           US-034819
                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-1996.
09-NOV-1995; U14673
                                                                                                                                                                                                                                                                                                                                                                                                           204 BP;
                                                                                                           30-MAR-1988; 105163
03-APR-1987; US-0348
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                     Lehtovaara P, Knowl
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 96-259862/26
                                                                                                                                                                                                                                                                                                                                                                                            See also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
W09615267-A1.
 Key
misc_feature
                                                     primer_bind
                                                                                  EP-285123-A
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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ID T2
AC T2
DT 02
DE PG
KW P5
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identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter.
Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococus. The method may also be used for the identification of viruses, especially hepatitis C virus and similar immunodeficiency virus. Fragments of the vector pGEM31 were used as a test sequence for the method. The fragments were used alongside test fragments of the
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostable 5' nuclease derived from thermostable polymerase - has reduced synthetic activity useful in nucleic acid detection assays Example 1C; Fig 21; 93pp; English. The ability of 5' nucleases derived from thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5' Nuclease(s) derived from thermostable DNA polymerase(s) - have cleavage activity with reduced synthetic ability, used for detection of specific target sequences.
Disclosure: Fig. 21; 159pp: English.
The ability of S' nucleases derived from thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA substrate for 5, nuclease.
DNA polymerase; 5' nuclease activity; DNA cleavage; RNA cleavage; transcleavage; hairpin structure; ss.
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                   Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-polymerase; DNAP; 5' nuclease; Thermus; DNA cleavage;
RNA cleavage; transcleavage; hairpin; ds.
                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-polymerases to cleave a specific sequence structure was tested using the present duplex sequence, and the pilot oligonucleotides given in 170337-39. Sequence 206 BP. 49 A; 48 C; 52 G; 57 T;
                                                                                                                                                                                                     57 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1006 TITCCCAGICAGGACGITGIAAAACGACGGCCAGIGAATIG 966
                                                                                                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                             4.69e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 37;
Pred. No. 4.69e-08;
                                                                                                                                                                                                                                                                                                                                                    10 tttcccagtcacgacgttgtaaaacgacggccagtgaattg
                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                     52 G;
                                                                                                                                                                                                                                                Score 39; DB 23
Pred. No. 4.69e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1994.
06-JUN-1994; U06253.
04-JUN-1993; US-073384.
(THIR-) THIRD WAVE TECHNOLOGIES INC.
Brow MAD, Dahlberg JE, Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
US5614402-A.
25-MAR-1997.
06-UUN-1994, 254359.
07-DEC-1992; US-986330.
04-UUN-1993, US-073384.
(THIR-) THIRD MAVE TECHNOLOGIES INC.
Brow MAD, Dahlberg UE, Lyamichev VI;
WPI; 97-201481/18.
                                                                                                                                                                                                     48 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
                                                                                                                                                                                                     49 A;
                                                                                                                                                                                                                                              3.9%;
Local Similarity 97.6%;
les 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.9%;
Best Local Similarity 97.6%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-1995 (first entry) 5' Nuclease substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T70340;
03-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .r 14
r70340 standard; DNA; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 15
Q80775 standard; DNA; 228
                                                                                                                                                                           human tyrosinase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brow MAD, Dahlber
WPI, 95-036504/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
WO9429482-A.
                                                                                                                                                                                                       Sequence
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DNA-polymerases to cleave a specific sequence structure was tested using the duplex sequence given in Q80775 and the pilot oligonucleotides given in Q80758-60. Sequence 228 BP; 59 A; 56 C; 53 G; 60 T;
88888
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ö 0; Gaps Length 228; Query Match 3.9%; Score 39; DB 13; Length 228; Best Local Similarity 97.6%; Pred. No. 4.69e-08; Matches 40; Conservative 0; Mismatches 1; Indels

Search completed: Fri May 14 08:09:48 1999 Job time : 166 secs.



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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm ou:

Fri May 14 07:16:35 1999; MasPar time 1611.89 Seconds 1474.893 Million cell updates/sec abular output not generated.

>US-08-911-423-3 (1-1006) from US08911423.seq 1006 Description: Perfect Score: N.A. Sequence: Comp: Title:

1 ATGGCACAGCACGGGGGGAT.....ACAACGTCCTGACTGGGAAA 1006 TACCGTGTCGTGCCCCGCTA.....TGTTGCAGGACTGACGTCTT

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 •• STD Nmatch 602357 segs, 1181590623 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in 7:em_on 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_un 15:em_vi genbank110

Database:

16:9b_bai 17:9b_ba2 18:9b_htg 19:9b_in 20:9b_om 21:9b_ov 22:9b_pat 23:9b_ph 24:9b_pli 25:9b_pi2 26:9b_pri 27:9b_pri 28:9b_pri 28:9b_pri 28:9b_pri 28:9b_pri 28:9b_pri 28:9b_pri 28:9b_pri 28:9b_pri 28:9b_pri 28:9b_rri 28:9b_rri

Mean 10.691; Variance 5.553; scale 1.925 tistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

						CHILDRIES		
			æ					
Result	1t		Query					
Ż	No.	Score	Match	Match Length DB	DB	ΙD	Description	Pred. No.
	-	228	22.7	1020	29	MMU82534	Mus musculus alucocort	7 350-151
ပ	7	116	11.5	4109	33	PSPORT1	Cloning vector psport1	1.956-63
U	m	106	10.5	4310	33	XXU12391	Cloning vector pSport2	7.72e-56
	4	82	8.4	1581	22	160018	Sequence 1 from patent	3.80e-40
	Ŋ	82	8.2	5772	24	SCU15970	Saccharomyces cerevisi	6.09e-38
ပ	9	70	7.0	2699	34	HIVU84854	HIV-1 strain MO2 from	3.04e-29
	7	9	6.8	86	27	HUMD4H12M3	Human HepG2 3' region	8.14e-28
	ω	63	6.3	538	22	AR023813	Sequence 1 from patent	2.80e-24
	σ	29	5.9	398	31	G13951	human STS SHGC-2867 cl	1.74e-21
	20	28	5.8	433	31	G41212	LSCV119 Caprine BAC Ca	8.55e-21
	1	27	5.7	3160	32	PSVSPORT	Cloning vector pSVSpor	4.19e-20
	12	26	5.6	1297	24	CSPATATLP	Cucumis sativus mRNA f	2.04e-19
	13	22	5.5	414	31	G14155	human STS SHGC-6182 cl	9.85e-19

9.85e-19 4.74e-18 5.04e-14 5.04e-14 4.68e-12 2.08e-11 1.72e-09	1.72e-09 7.32e-09 7.32e-09	3.08e-08 3.08e-08 3.08e-08	3.08e-08 3.08e-08 3.08e-08	08e- 08e- 08e-	086-0 086-0 086-0 086-0
Cloning vector pGEM-42 human STS SHGC-3196 cl human STS SHGC-3135 cl Sequence 14 from paten Mus saxicola haptoglob Sequence 22 from paten Sequence 5 from paten LSCV116 Caprine BAC Ca	14 from ector p ector p ta910.	Cryptosporidium parvum pBluescript KS(+) vect pBluescript SK(+) vect	vector vector vector is gene cloning	Arabidopsis thaliana g Cloning vector pJB3, c pmTv1 DNA sequence. Expression vector pBSI Cloning vector pYEUra3	H 0
CVPGEM42 G16894 G17976 I66494 MUSHAPTGB AR024229 I28278 G41210	166494 AF017063 ECY10544 A04663	CPU69698 ARBLKSP ARBLSKP	CVGEM112P CVU39779 PL18SRNA XXU13848	ATHAVPEA CVU73899 A20700 EVU84006 U02457	SYNPHSCSKV CVU51113 D78345 AC002317 CEY66C5 HS437G10
322 331 32 32 32 32 32 32 32 32 32 32 32 32 32	32 32 16 22	3222	22622	33334	18 18 18 18
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ALIGNMENTS

MMU82534 1020 bp mRNA ROD 18-OCT-1997 Mus musculus glucocorticoid induced TNFR family related protein UR2534 92228583	house mouse. Mus musculus Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	<pre>1 (bases 1 to 1020) Nocentini,G., Giunch).L., Ronchetti,S., Krausz,L.T., Bartoli,A., Noraca,R., Migliorati,G. and Riccardi,C. A new member of the tumor necrosis factor/nerve growth factor A new member is thiniting not a processis factor family.</pre>	receptor radilly inhibits i cell receptor-induced apoptosis proc. Natl. Acad. Sci. U.S.A. 94 (12), 6216-6221 (1997) 2 (bases 1 to 1020) Nocentini, G., Giunchi, L., Ronchetti S., Krausz, L.T., Bartoli, A., Moraca, R., Migliorati, G. and Riccardi, C.	Submitted (18-DEC-1996) Carlo Riccardi, Clinical Medicine, Pathology and Pharmacology, Perugia University, V. del Glochetto, Perugia, PG 06100, Italy Location/Qualifiers	11020 /organism="Mus musculus" /strain="C3H/HeN" /db_xref="taxon:10090" /db_type="thymocytes" /orde="type I transmembrane protein; belongs to the tumor necrosis factor receptor/nerve growth factor receptor family" /codon_start=1 /product="glucocorticoid induced TNFR family related
RESULT 1 LOCUS MM DEFINITION MU ACCESSION UB NID 92 KEYWORDS	Σ	REFERENCE 1 AUTHORS NO TITLE A	JOURNAL PE MEDLINE 97 REFERENCE 2 AUTHORS NO	J s	Source

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                                                                      MAACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTE
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CAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLV
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/note="type I transmembrane protein"
/product="glucocorticoid induced TNFR family
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Pred. No. 2.35e-151;
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/note="encodes TNFR cystein repeat 1"
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/note="encodes transmembrane domain"
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/note="encodes extracellular domain"
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/note="encodes
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23-AUG-1994

UNA

Cloning vector pSportl, complete cds. U12390 9531828

DEFINITION ACCESSION NID

4109 bp

PSPORT1

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/evidence=experimental
/product="lac repressor"
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LNYIPNRVAQQLAGKQSLLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERS
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IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE
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FSHBEGTRLOVBHLYALGAQIALLAGPLSSVSARIRAGAHKYLTRNOIQPIARREG
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EDSSCYIPPSTTIKQDFRLLGQTSVDRLLQLSQGAVKGNQLLPVSLVKRYTILAPNT
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complement(125. .147)
/standard_name="M13/pUC 23 base forward sequencing primer"
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D'Alessio,J.M., Gruber,C.E., Cain,C. and Noon,M.C.
Construction of Directional cDNA Libraries Using the Superscript
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/evidence-experimental
164..180
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Technical Services, 8400 Helgerman Court, Gaithersburg, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Cloning vector pSportl"
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/standard_name="ORI E. coli
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                                                                 artificial sequence; cloning vectors
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191. .285
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/codon_start=1</pre>
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Direct Submission
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US-08-911-423-3.rge

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LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (sites) Gruber, C.E., Li, W., Lin, J. and D'Alessio, J.M. Subtractive cDNA hybridization using the multifunctional plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Horton,M.E.
Direct Submission
Submitted (18-JUL-1994) Mary E. Horton, Life Technologies, Inc.,
Technical Services, 8400 Helgerman Court, Gaithersburg, MD
                                                                                                                                                                                                                                    122 TITCCCAGICA¢GACGIIGTAAAACGACGGCCAGIGAATIIGAAITIAGGIGACACIAIAG 181
                                                                                                                                                                                                                                                                                   AGAGGGGCGCCGA 241
                                                                                                                                                                                                                                                                                                24-MAY-1995
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(125. .147)
/note="M13/pUC 23 base forward sequencing primer"
complement(150. .161)
/note="M13/pUC forward sequencing primer"
                                                                                                                                                                                        ó
                                                                                                                                                          Length 4109;
                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                 182 AAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTTGGATCCT
                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Cloning vector pSport2"
/plasmid="pSport2"
/db.xref="taxon:36587"
/lab_host="Escherichia coli"
complement(<1...344)
                                                                                                                                                                                                                                                                                                                                                                     XXU12391 4310 bp DNA UNO CLONING Vector pSport2, complete sequence. U12391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="multiple cloning site"
                                                                                                                                                       Score 116; DB 33;
Pred. No. 1.95e-63;
0; Mismatches 2;
                                                          3667. .4109 /note="F1 intergenic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning vector pSport2.
Cloning vector pSport2
artificial sequence; cloning vectors.
                                                                                         /evidence=experimental
1064 c 1062 g
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/note="T7 promoter"
/evidence=experimental
complement(467. .1549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SP6 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector pSport2
Focus 15 (3), 59-65 (1993)
2 (bases 1 to 4310)
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/transl_table=11
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                                                                                                                                                       11.5%;
ilarity 98.3%;
Conservative
                                            EIGASLIKHW"
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                                                                                                                                                                       l Similarity
118; Conserv
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                                                             rep_origin
                                                                                                                                                       Query Match
Best Local 9
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ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                              RESULT
LOCUS
                                                                                                                          ORIGIN
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/evidence=experimental
/product="Lac repressor"
/d_xxef="P1D: 95318X4
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DWASANGSFQOTMQMLNESIVPTAMLVANDQMALGAMRAITESGLRVGADISVVGYDDT
EDSSCYIPPLTTIKOPRLLAGDTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNT
QTASPRALADSLMQLARQVSRLESGQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IELDLNSGKILESFRPEERFPMASTFKVLLCGAVLSRIDAGQEOLGRRIHYSONDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTWPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
                                                                                                                                                                         GVEACKAAVHNLLAQRVSGLIINYPLDDQDAIAVEAACTNVPALFLDVSDQTPINSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRSALPAGWF1ADKSGAGERGSRG11AALGPDGKPSR1VV1YTTGSQATMDERNRQ1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 TTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGAATTTAGGTGACACTATAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1006 TTTCCCAGTCAGGACGTTGTAAAACGACGCCAGTGAATTGAATTTAGGTGACACTATAG 947
                                                                                                                                                                                                                                                                                               complement(1896. .1902)
/standard_name="ORI E. coli pMB1 (ColE1 and pBR322)"
/evidence=experimental
complement(2706. .3566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-1997
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/transl_except=(pos:complement(1547. .1549),aa:Met)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1581;
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                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/function="ampicillin resistance"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 106; DB 33; I
Pred. No. 7.72e-56;
0; Mismatches 2;
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Pred. No. 3.80e-40;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of myristate in plant cells
Patent: US 5654495-A 1 05-AUG-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIGASLIKHW"
3667. .4109
/note="F1 intergenic region"
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Voelker,T.Alois and Davies,H.Maelor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="beta-lactamase"
/db_xref="PID:9531835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1 from patent US 5654495.
160018
92478650
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356 c 410 g
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                         /transl_table=11
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RESULT

Dp

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DEFINITION

ACCESSION

SOURCE ORGANISM

KEYWORDS

RENCE HORS

JOURNAL MEDLINE

AUTHORS JOURNAL

TITLE

REFERENCE

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lentivirus group.

1 (bases I to 2699)

2 (chases I to 2699)

Walker, B. D., Neumann, A. U., Vermund, S. H., Mestecky, J., Jackson, S., Fenamore, E., Cao, Y., Gao, F., Kalams, S., Kunstman, K. J., McDonald, D., McWilliams, M., Trkola, A., Moore, J. P. and Wolinsky, S. M. Immunological and virological analyses of persons infected by human immunodeficiancy virus type I while participating in trials of Trecombinant gpl20 subunit vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTONTTENHTLEPCRINGIINWQEVGNAMYAPPIRGQIRCKSNITGLLLTREGGENTN
HTDNNTEIFREGGEDMRDNWRSELKYKVWIEPLGYAPTRARRENVOREKRAVGIGA
MFLGFLGAGGSTWGAASTULVQARLLLSGIVQQSNLLRAIEAQOHLLQUTVWGIRG
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EISNYTVLKYSIIESONOQEKNELELLELDKWASLWNWFDITNWLWYIKIINVJGG
LVGLRIVLSTVLNYSROGYSPLSFOTTREPTREPDREGEIEEDGERDKDRSIRLY
DGFLALIWDDLRSLCEFSYHRLRDLLIVELLGRRGWEALKYWGNLIQYWIQELKKSA
ISLLNATAIVVABGTDRAIEALQTAGRAILHIPRRIRQGLERALL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APAGFAILKCNNKTFSGKGPCTNVSTVQCTHGIRPVYSTQLLLNGSLAEKEVIIRSDD
FSDNTKTIIVQLNESVAIDCIRPSNNTRKSIHIGPGRAFYATGTIIGDIRQAHCTINR
TQMNQTLDRVIRKLKKQFVNKEIEFKGSSGGDPEIVMHSVNCGGEFFYCNTTQLFNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:11676"
/note="subtype B; PBMC from an early vaccine-break control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="envelope glycoprotein"
/db_xref="PID:g2290121"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WKEATTTLFCASDAKAYDTERHNVWATHACVPTDPNDGEVLLENVTENFNWKNNMVE
QMHEDIISLWDQSLKPCVKLTPLCVTLNCTDVTLNSTGVNVTNELKNLTNEMKNCSFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITTNIRDKIKKEYALFYTLDIVPIDNSNDSYRLISCNTSVITQACPKVTFEPIPIHYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-JAN-1997) HIV Database, Los Alamos Nat'l Labs, Mail Stop K710, Los Alamos, NM 87545, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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/organism="Human immunodeficiency virus type
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Pred. No. 3.04e-29; 0; Mismatches 1
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/db_xref="PID:92290122"
/translation="MGGKWSKSSVVG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         644 t
                                                                                                       Human immunodeficiency virus type 1.
Human immunodeficiency virus type 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2699)
Wolinsky, S. and Hahn, B.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="MO2"
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/gene="nef"
2663. .>2699
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/gene="env"
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/gene="env"
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Best Local Similarity 98.6%;
Matches 71; Conservative
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  partial cds.
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JOURNAL
                             ACCESSION
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REFERENCE
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RYISIVWILWLGLISYYESVVVKRAMKKCQWSTWEDWPEGAESHRVGLFADPQIMDEY
SYPGRPQIVNYFTRVIVDHYHRRNWKYVQYYLDPDSNFFLGDLFDGGRNWDDKQWIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (13-OCT-1994) Nathan Nelson, Roche Institute of Molecular
Biology, 340 Kingsland St., Nutley, NJ 07110, USA
Location/Qualifiers
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VLLDTISLSKTNPNYSRVPRGFLDNRAMGSHPLPRLILTHYPLMRDPEQOTGGQLRE
SYEPPF JOKGHQYQYTVIENDISOELTHKIQPEILFSGDDHDHCQISHSYPFGGKTKNA
QEITYKSCAMMGISRAJQLLSLYNPSDLTWNMAGETSASKTYQTELCYMPDPYKAI
RMYLMGLLFSAAFIAYMHFFPKSFNNRVATIMNRVFTRPDGNTSDLPLDFSISKSKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CDC1; similar to S. cerevisiae CDC1 gene product, encoded by GenBank Accession Number X81813"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1.05772)
Supek,F., Supekova,L., Nelson,H. and Nelson,N.
A yeast manganese transporter related to the macrophage protein involved in conferring resistance to mycobacteria Proc. Natl. Acad. Sci. U.S.A. 93 (10), 5105-5110 (1996)
889 GGCGCCGCTCTAAAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCTTCT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1998
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DEFINITION HIV-1 strain MO2 from USA, envelope glycoprotein (env) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5642 TACAAGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCTTCTATAGTGTCACC
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                  Hemiascomycetes; Saccharomycetales; Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSLTHSKYAVNDTRSIKQFLVNAIVLEVSVMPIFIYFYTVV"
1015 c 1053 g 1875 t
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                                                                                                                                                                                       SCUIS970 5772 bp DNA PLN Saccharomyces cerevisiae CSP2 gene, complete cds. U15970

    5772
/organism="Saccharomyces cerevisiae"
/strain="W303"

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Pred. No. 6.09e-38;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SGD:L0000241"
2462. .3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/db_xref="SGD:L0000241"
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2462. .3937
/gene="CSP2"
                                                  1555 ATAGTGTCACCTAAATTCAATTCACTG 1581
                                                                             949 ATAGTGTCACCTAAATTCAATTCACTG 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'function="unknown"
                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae
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Nelson, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.2%;
Best Local Similarity 90.7%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                     baker's yeast.
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FEATURES

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9 Gaps

61 AGAGGGGCCGCC 72

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RESULT

BASE COUNT ORIGIN

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2; Gaps

22-DEC-1995

DEFINITION

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ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

REFERENCE

AUTHORS TITLE

JOURNAL

COMMENT

ERENCE

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 2 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue
                                                                                                                                                                                                               441 GCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATNN-TCTTCTT 499
                                                                                                                                                                                                                                                 94 degrees C for 15 seconds 62 degrees C for 23 seconds 72 degrees C for 30 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259689
                                                                                                                                Length 538;
                                                                           8 others
                                                                                                                                Score 63; DB 22; Length 538
Pred. No. 2.80e-24;
0; Mismatches 11; Indels
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Perkin Elmer 9600
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STS sequence; primer; sequence tagged site.
human.
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                                                                                                                                                                                                                                                                                        500 TAGTGTCAACCTAAATCAAT-CANTGGCCGCCGGTT 534
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each 1 uM
each 200 uM
0.05 units/ul
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Patent: US 5795740-A 1 18-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                   G13951 398 bp DNA
human STS SHGC-2867 clone pG-564.
G13951
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50 mM
20 mM
8.3
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                                                       /organism="unknown"
123 c 137 g
                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dNTPs:
Taq Polymerase:
Total Vol:
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Polymerization:
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                                                                                                                                  Query Match 6.3%;
Best Local Similarity 86.5%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1995)
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PCR Profile:
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ORGANISM
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                                                                             BASE COUNT
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JOURNAL
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                   FEATURES
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                                                                                                                                                                                                                                                                                                      Matoba,R., Okubo,K., Hori,N., Fukushima,A. and Matsubara,K.
The addition of 5'-coding information to a 3'-directed cDNA library improves analysis of gene expression
Gene 146 (2), 199-207 (1994)
94357437
                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo
Matoba, Osaka University, Institute for Molecular and Cellular Bio;
1-3, Yamada-oka, Suita, Osaka 565, Japan
(E-mail:matoba@inherit.incb.osaka-u.ac.jp,
Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922)
Submitted (21-Jul-1993) to DDBJ by:
                                                                                                                                                                          gene signature.
Homo sapiens Male cell_line:HepG2 cDNA to mRNA, clone_lib:Kiseru.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Microbiology and Genetics Lab.
Research Institute of Innovative Technology for the Earth 9-2
Scraku-gun, Kizu-cyo,
Soraku-gun, Kyoto.
Japan, 619-02
Phone: 07747-5-2308
Fax: 07747-5-2321.
                                                                                              01-DEC-1994
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Platica,M., Platica,O. and Holland,J.F.
Pituitary differentiation factor and methods of use thereof
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                                                                             HUMD4H12M3 98 bp mRNA PRI
Human HepG2 3' region MboI cDNA, clone hmd4h12m3.
D17247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
/clone_lib="Kiseru"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1 from patent US 5795740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ery Match 6.8%;
est Local Similarity 87.6%;
latches 78; Conservative
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               900 AGAGGGGCCGCC 889
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Matoba, R
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FEATURES

BASE COUNT

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Matches

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RESULT LOCUS

DEFINITION

ACCESSION NID KEYWORDS ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

9

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/evidence-experimental
/product="beta-lactamase"
/d_xref="plis-g540253"
/translation="%XIGHERVALIPFFAAPCLPVFAHPETLVKVKDAEDOLGARVGY
IELDLNSGKILLESFRPEERFPMMSTFKVLLCGAVLSRIDAGGEQLGRRIHYSQNDLVE
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                      /strain="Saanen"
/note="Vector: pBeloBAC11; V-type: BAC; Genomic HindIII
fragments (average size 150 kb)"
/db.xref="taxon:9925"
/clone_lib="Caprine BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-SEP-1994) Mary E. Horton, Life Technologies, Inc., Technical Services, 8400 Helgerman Court, Gaithersburg, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 TTCTATAGTGTCACCTAAATCCAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGA 351
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Score 58; DB 31; Length 433;
Pred. No. 8.55e-21;
0; Mismatches 2; Indels

    .3160
    /organism="Cloning vector pSVSportl"
/db_xref="taxon:40160"

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Cloning vector pSVSport1
artificial sequence; cloning vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Life Technologies, Inc. Catalogue Unpublished (1994)
C (1988)
Horton, M.E.
Direct Submission
                                                       /organism="Capra hircus"
                                                                                                                                                                                /tissue_type="skin"
/cell_type="fibroblast"
/cell_line="CAT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2003. .2863)
Chromosome localization : 1943.
Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                             complement(206.
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                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.8%;
Best Local Similarity 96.8%;
Matches 60; Conservative
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polyA_signal
rep_origin
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primer_bind
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AUTHORS
TITLE
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NID
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                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 433)
Vaiman, D., Schibler, L., Oustry-Vaiman, A., Pailhoux, E., Furet, J.-P.,
Vaiman, D., Schibler, L., Schwerin, M., Fellous, M. and Cribiu, E.P.
High-resolution human/go, schwerin, M., Fellous, M. and Cribiu, E.P.
High-resolution human/got comparative map of the goat
Polled/Intersex Syndrome (PIS): The human homologue is contained in
unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                      G41212 433 bp DNA STS 19-AUG-1998
LSCV119 Caprine BAC Capra hircus STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratoire de Genetique biochimique et de Cytogenetique
Institut National de la Recherche Agronomique
Centre de Recherche INRA de Jouy-en-Josas, 78352 Jouy-en-Josas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer: each 1 uM
dGTP, dCTP, dTTP: 100mM, dATP: 10mM + alpha P33 dATP 0.5 uCi
Taq Polymerase: 0.05 units/ul
                                                                                                                                                                                                                  320 GGCGGNCNCTCTAGAGGATCCAAGCTTACGTACGCGTGCAINCGANGTCATAG-TCTTCT 378
                                                                                                                                                                                                                                         goat.
Capra hircus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae;
                                                                                                                                                                                   Gaps
                                                                                                                                             Score 59; DB 31; Length 398;
Pred. No. 1.74e-21;
0; Mismatches 8; Indels
                                                                                         10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Denaturation: 94 oC for 15 seconds
Annealing: 58 oC for 20 seconds
Polymerization: 72 oC for 20 seconds
PCR CYCLES: 30
Thermal cycles: MJ Research or Perkin-Elmer Cetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 33134652672
Fax: 33134652478
Email: cribiu@biotec.jouy.inra.fr
Primer A: CAAGCTACAGTCTATAGGGTC
Primer B: CTACACTGGCCAGAGGATTC
STS size: 155
PCR Profile:
               /organism="Homo sapiens
                                110. .241
110. .132
complement(219. .241)
a 83 c 100 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presoak: 94 oC for 5 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Edmond P. Cribiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Template: 30-100 ng
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Tween20: 0.01% w/v
Tris-HCl: 75 mM
                                                                                                                                         Local Similarity 88.2%;
tes 67; Conservative
                                                                                                                                                                                                                                                                                           379 NTNGTGTCAACTAAAT 394
                                                                                                                                                                                                                                                                                                                949 ATAGTGTCACCTAAAT 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MgC12: 2 mM
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g3435060
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BASE COUNT
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                                                                                                                                               Query Match
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source
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Matches
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COMMENT
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BASE COUNT

12

RESULT

අ ò DEFINITION

SSION

MORDS

SOURCE

ORGANISM

AUTHORS TITLE

REFERENCE

REFERENCE AUTHORS JOURNAL

TITLE

JOURNAL

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Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 15 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue for Medical Research, Camden, NJ 08103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 GGCGGCCGTTCTNGAGGATCCAAGCTTACGTACGCGTGCATGCGACGNCATAGGCTCTNC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-1996
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                                                                                                                                                                                                                                        Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259689
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 31; Length 414
Pred. No. 9.85e-19;
0; Mismatches 8; Indels
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23
30
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degrees C for 2
degrees C for 3
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                   STS sequence; primer; sequence tagged site.
human.
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0.05 units/ul
10 ul
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76. .196
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72
30
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87 g
                                                                                                                                                                                                                                                                                                                                                     Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                           Primer A: TCCCACAACAGTAAAGGAG
Primer B: CAAGGTATGGTGACGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     쥩쥩줱
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Location/Qualifiers
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20
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8.3
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Polymerization:
PCR Cycles:
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Taq Polymerase:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.5%;
Best Local Similarity 87.2%;
Matches 82; Conservative
                                                                                                                                                                                                      Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                              STS size: 121
PCR Profile:
                                                                                                                                                                                       Myers, R.M.
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ORGANISM
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 ACCESSION
                                                                                                                                                                      REFERENCE
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                                    KEYWORDS
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//db_xref="PID: 92462266"
//translation="PRVRFLSLFVLLTMVADFAKGKMITILSIDGGGIRGIIPSIILA
FLESKLQELDGPDVRIADYFDVIAGTSTGGLVTSMLTAPDKNNRPLYSASDLALFYIE
HAPKIFPQRNYFLCSLVNFFGKVMGPRXNGLYLRSLIKGLLGDITLKQTLSQVVIPAF
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
LRWEPELINEAIPNDERDTTMPVAMATTIRKLLTGELLTLASRQQLIDWREDKYAGPL
LRSALPAGKTIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIKLLOPVIFTTIEAKCSELKNPKLADVCISTSAAPTFLPGYEFQTKDSKGNIRNYEM
VOGGYAANNPTLAAMTHVYKEMSILTRHRSELLKIKPMETERMLVLSLGTGTPKNDEKY
SAARASKWGMLDWYYHGGGTPIVDIFSDASADMVDYH SSIFQSDHCHKNYLRIQDDT
LSGEVSSVDIATEENLLINLIYYGENLLKKPLSRVNLESGKFEPLDARGTNRQALABERA
                                                                                                                                                                                                                                                                                                                                                                                                                          Cuccumis sativus

Eukaryoteae, Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; vascular plants; seed plants; Magnoliophyta;

Magnoliopsida; Violales; Cucurbitaceae; Cucumis.

1 (bases 1 to 1297)

1 (bases 1 to 1297)

1 the partain-like protein localized to lipid bodies involved in the mobilization of fat reserves?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-APR-1997) H. Kindl, FB Chemie Universitaet Marburg,
Hans-Meerwein-Strasse, 35043 Marburg, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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/function="mobilization of fat during seed germination"
                                                                                                                                                                                                                                                                                                               CSPATATLP 1297 bp RNA PLN 30-SEP-1997 Cucumis sativus mRNA for patatin-like protein, partial. Y12793
                                                                                                                                                                                                                         22-DEC-1995
                                                                                                                                                                                                    416 TCGGCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGCCCCTCTAGAGGATCCAAGCTTACGTACGCGTGCATGCGACGTCATAGCTCTT 1297
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                                                                                                                            Score 57; DB 32; Length 3160;
Pred. No. 4.19e-20;
0; Mismatches 1; Indels
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/db_xref="PID:e316871"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 24; I
Pred. No. 2.04e-19;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Cucumis sativus"
/db_xref="taxon:3659"
/tissue_type="cotyledon"
/clone_lib="psporr"
/clone="cshsp70291"
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DEFINITION human STS SHGC-6182 clone pg-2782.
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                                                                                                                            Query Match 5.7%;
Best Local Similarity 98.3%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 5.6%;
Local Similarity 98.3%;
les 57; Conservative
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source

FEATURES

CDS

Gaps

Query Match

Matches

1240

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BASE COUNT ORIGIN

13

RESULT

948

05-MAR-1996

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DEFINITION ACCESSION

KEYWORDS

SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL

TITLE JOURNAL

IN

AUTHORS

REFERENCE

REMARK

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Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amilota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                      STS sequence; primer; sequence tagged site.

human Plasmid clones, generated from a lymphoblastoid cell line
trom a human male. Localized to human chromosome 5 by analysis on
the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell
Institue for Medical Research, Camden, NJ 08103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1006 TITCCCAGTCAGGACGTTGTAAAACGACGCCCAGTGAATTGAATTTAGGTGACACTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 390;
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Pred. No. 4.74e-18;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C for 15 s
C for 23 s
C for 30 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 degrees C for 15
64 degrees C for 23
72 degrees C for 30
30
Perkin Elmer 9600
                                                                                               STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  each 1 uM
each 200 uM
0.05 units/ul
10 ul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer A: TIGITGATGATCTGCGATATGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                                                             G16894 390 bp DNA
human STS SHGC-3196 clone pG-1108.
G16894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer B: GGCCAAAAAAGCGAAGCTCCATC
STS size: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       골돌
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      пg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Richard M. Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymerization:
PCR Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taq Polymerase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.4%;
Best Local Similarity 85.7%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annealing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86. .215
86. .110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tris-HCl:
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                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Profile
                                                                                                                                                                                                                                                                                                                                                                                       Myers, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STS size:
PCR Profil
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primer_bind
                                                                                                               DEFINITION
ACCESSION
                                                                           15
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                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                   NID
KEYWORDS
SOURCE
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                                                                           RESULT
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YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTWPVAMPTTLRKLLTGELLTLASRQOLIDWMEADKVAGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (28-MAY-1993) Technical Services, Promega Corporation,
2800 Woods Hollow Road, Madison, Wi 53711-5399, USA
This vector can be obtained from Promega Corporation, Madison, WI.
Call one of the following numbers for order or technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                          Submitted (23-MAR-1992) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2688 TITCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGGATTTAGGTGACACTATA 2746
                                                         gene; cloning vector; lac2 gene; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="SP6 transcription initiation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="T7 transcription initiation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                           //sconsin 800-356-9526
//side U.S. 608-274-4330
<X65300-X65335> for related vector sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 32; 1 Pred. No. 9.85e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7. .63
/note="multiple cloning sites"
                                                                     cloning site; promoter.
unidentified cloning vector.
unidentified cloning vector
artificial sequence; cloning vectors.
1 (bases 1 to 2746)

 Mismatches

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/note="lac operon sequence"
2729. .2746
/note="SP6 promoter"
681 c 703 g 679 t
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/note="lac operon sequence"
complement(108. .110)

    .2746,
    /organism="Cloning vector"
    /plasmid="Plasmid pGEM"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/product="Beta-lactamase"
/db_xref="PID:958208"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="lacz"
/note="lacz start codon"
complement(108. 110)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Order or Technical 800-356-9526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130. .146
/note="lac operator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="T7 promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
 Cloning vector pGEM-4Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="lacz"
130. .146
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Best Local Similarity 96.6%;
                                                                                                                                                                                                                                                    ised by [2]
(bases 1 to 2746)
                                                       beta-lactamase; bla
                                                                                                                                                                      Technical, Services.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Wisconsin
                                                                                                                                                                                                                                                revised by
                                                                                                                                                                                                                                                                                                                                                                                                         information
                                                                                                                                                                                                                                                                                        Klock, C.
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Matches

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Search completed: Fri May 14 07:43:41 1999 Job time : 1626 secs.